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TECH CENTER 1600/2900

RAW SEQUENCE LISTING

DATE: 01/27/2004

PATENT APPLICATION: US/09/774,681A

TIME: 13:12:59

Input Set : A:\4835579d.app

Output Set: N:\CRF4\01272004\I774681A.raw

3 <110> APPLICANT: SHERMAN, LINDA A.
 4 LUSTGARTEN, JOSEPH
 6 <120> TITLE OF INVENTION: RECOMBINANT CONSTRUCTS ENCODING T CELL RECEPTORS
 7 SPECIFIC FOR HUMAN HLA-RESTRICTED TUMOR ANTIGENS
 9 <130> FILE REFERENCE: 48340/55793-DIV
 11 <140> CURRENT APPLICATION NUMBER: 09/774,681A
 12 <141> CURRENT FILING DATE: 2001-02-01
 14 <150> PRIOR APPLICATION NUMBER: 08/812,393
 15 <151> PRIOR FILING DATE: 1997-03-05
 17 <150> PRIOR APPLICATION NUMBER: 60/012,845
 18 <151> PRIOR FILING DATE: 1996-03-05
 20 <160> NUMBER OF SEQ ID NOS: 64
 22 <170> SOFTWARE: PatentIn Ver. 2.1
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 1350
 26 <212> TYPE: DNA
 27 <213> ORGANISM: Artificial Sequence
 29 <220> FEATURE:
 30 <221> NAME/KEY: CDS
 31 <222> LOCATION: (1)..(1332)
 33 <220> FEATURE:
 34 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 35 single chain TCR derivative nucleotide sequence
 37 <400> SEQUENCE: 1
 38 ctc gag atg cag agg aac ctg gga gct gtg ctg ggg att ctg tgg gtg 48
 39 Leu Glu Met Gln Arg Asn Leu Gly Ala Val Leu Gly Ile Leu Trp Val
 40 1 5 10 15
 42 cag att tgc tgg ctg aaa gaa cag caa gtg cag cag agt ccc gca tcc 96
 43 Gln Ile Cys Trp Leu Lys Glu Gln Gln Val Gln Gln Ser Pro Ala Ser
 44 20 25 30
 46 ttg gtt ctg cag gag ggg gag aac gca gag ctc cag tgt agc ttt tcc 144
 47 Leu Val Leu Gln Glu Gly Glu Asn Ala Glu Leu Gln Cys Ser Phe Ser
 48 35 40 45
 50 atc ttt aca aac cag gtg cag tgg ttt tac caa cgt cct ggg gga aga 192
 51 Ile Phe Thr Asn Gln Val Gln Trp Phe Tyr Gln Arg Pro Gly Gly Arg
 52 50 55 60
 54 ctc gtc agc ctg ttg tac aat cct tct ggg aca aag cag agt ggg aga 240
 55 Leu Val Ser Leu Leu Tyr Asn Pro Ser Gly Thr Lys Gln Ser Gly Arg
 56 65 70 75 80
 58 ctg aca tcc aca aca gtc att aaa gaa cgt cgc agc tct ttg cac att 288
 59 Leu Thr Ser Thr Thr Val Ile Lys Glu Arg Arg Ser Ser Leu His Ile
 60 85 90 95
 62 tcc tcc tcc cag atc aca gac tca ggc act tat ctc tgt gcc tca aat 336

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63 Ser Ser Ser Gln Ile Thr Asp Ser Gly Thr Tyr Leu Cys Ala Ser Asn
64      100      105      110
66 tct gga gga agc aat gca aag cta acc ttc ggg aaa ggc act aaa ctc 384
67 Ser Gly Gly Ser Asn Ala Lys Leu Thr Phe Gly Lys Gly Thr Lys Leu
68      115      120      125
70 tct gtt aaa tca ggt ggc gga ggg tct ggc ggg ggt gga tcc ggg ggt 432
71 Ser Val Lys Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
72      130      135      140
74 gga ggc tca gag gct gca gtc acc caa agc cca aga aac aag gtg gca 480
75 Gly Gly Ser Glu Ala Val Thr Gln Ser Pro Arg Asn Lys Val Ala
76 145      150      155      160
78 gta aca gga gga aag gtg aca ttg agc tgt aat cag act aat aac cac 528
79 Val Thr Gly Gly Lys Val Thr Leu Ser Cys Asn Gln Thr Asn Asn His
80      165      170      175
82 aac aac atg tac tgg tat cgg cag gac acg ggg cat ggg ctg agg ctg 576
83 Asn Asn Met Tyr Trp Tyr Arg Gln Asp Thr Gly His Gly Leu Arg Leu
84      180      185      190
86 atc cat tat tca tat ggt gct ggc agc act gag aaa gga gat atc cct 624
87 Ile His Tyr Ser Tyr Gly Ala Gly Ser Thr Glu Lys Gly Asp Ile Pro
88      195      200      205
90 gat gga tac aag gcc tcc aga cca agc caa gag aac ttc tcc ctc att 672
91 Asp Gly Tyr Lys Ala Ser Arg Pro Ser Gln Glu Asn Phe Ser Leu Ile
92      210      215      220
94 ctg gag ttg gct acc ccc tct cag aca tca gtg tac ttc tgt gcc agc 720
95 Leu Glu Leu Ala Thr Pro Ser Gln Thr Ser Val Tyr Phe Cys Ala Ser
96 225      230      235      240
98 ggt gag aca ggg acc aac gaa aga tta ttt ttc ggt cat gga acc aag 768
99 Gly Glu Thr Gly Thr Asn Glu Arg Leu Phe Phe Gly His Gly Thr Lys
100      245      250      255
102 ctg tct gtc ctg act agt aac tcc atc atg tac ttc agc cac ttc gtg 816
103 Leu Ser Val Leu Thr Ser Asn Ser Ile Met Tyr Phe Ser His Phe Val
104      260      265      270
106 ccg gtc ttc ctg cca gcg aag ccc acc acg acg cca gcg ccg cga cca 864
107 Pro Val Phe Leu Pro Ala Lys Pro Thr Thr Thr Pro Ala Pro Arg Pro
108      275      280      285
110 cca aca ccg gcg ccc acc atc gcg tcg cag ccc ctg tcc ctg cgc cca 912
111 Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro
112      290      295      300
114 tct agt tct aga gat ccc aaa ctc tgc tac ctg ctg gat gga atc ctc 960
115 Ser Ser Ser Arg Asp Pro Lys Leu Cys Tyr Leu Leu Asp Gly Ile Leu
116 305      310      315      320
118 ttc atc tat ggt gtc att ctc act gcc ttg ttc ctg aga gtg aag ttc 1008
119 Phe Ile Tyr Gly Val Ile Leu Thr Ala Leu Phe Leu Arg Val Lys Phe
120      325      330      335
122 agc agg agc gca gac gcc ccc gcg tac cag cag ggc cag aac cag ctc 1056
123 Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu
124      340      345      350
126 tat aac gag ctc aat cta gga cga aga gag gag tac gat gtt ttg gac 1104
127 Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp

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128          355          360          365
130 aag aga cgt ggc cgg gac cct gag atg ggg gga aag ccg aga agg aag 1152
131 Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys
132          370          375          380
134 aac cct cag gaa ggc ctg tac aat gaa ctg cag aaa gat aag atg gcg 1200
135 Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala
136 385          390          395          400
138 gag gcc tac agt gag att ggg atg aaa ggc gag cgc cgg agg ggc aag 1248
139 Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys
140          405          410          415
142 ggg cac gat ggc ctt tac cag ggt ctc agt aca gcc acc aag gac acc 1296
143 Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr
144          420          425          430
146 tac gac gcc ctt cac atg cag gcc ctg ccc cct cgc taa gcg gcc gcc 1344
147 Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
148          435          440
150 acc gcg 1350
153 <210> SEQ ID NO: 2
154 <211> LENGTH: 444
155 <212> TYPE: PRT
156 <213> ORGANISM: Artificial Sequence
158 <220> FEATURE:
159 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
160 single chain TCR protein
162 <400> SEQUENCE: 2
163 Leu Glu Met Gln Arg Asn Leu Gly Ala Val Leu Gly Ile Leu Trp Val
164 1 5 10 15
166 Gln Ile Cys Trp Leu Lys Glu Gln Gln Val Gln Gln Ser Pro Ala Ser
167 20 25 30
169 Leu Val Leu Gln Glu Gly Glu Asn Ala Glu Leu Gln Cys Ser Phe Ser
170 35 40 45
172 Ile Phe Thr Asn Gln Val Gln Trp Phe Tyr Gln Arg Pro Gly Gly Arg
173 50 55 60
175 Leu Val Ser Leu Leu Tyr Asn Pro Ser Gly Thr Lys Gln Ser Gly Arg
176 65 70 75 80
178 Leu Thr Ser Thr Thr Val Ile Lys Glu Arg Arg Ser Ser Leu His Ile
179 85 90 95
181 Ser Ser Ser Gln Ile Thr Asp Ser Gly Thr Tyr Leu Cys Ala Ser Asn
182 100 105 110
184 Ser Gly Gly Ser Asn Ala Lys Leu Thr Phe Gly Lys Gly Thr Lys Leu
185 115 120 125
187 Ser Val Lys Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
188 130 135 140
190 Gly Gly Ser Glu Ala Ala Val Thr Gln Ser Pro Arg Asn Lys Val Ala
191 145 150 155 160
193 Val Thr Gly Gly Lys Val Thr Leu Ser Cys Asn Gln Thr Asn Asn His
194 165 170 175
196 Asn Asn Met Tyr Trp Tyr Arg Gln Asp Thr Gly His Gly Leu Arg Leu
197 180 185 190

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199 Ile His Tyr Ser Tyr Gly Ala Gly Ser Thr Glu Lys Gly Asp Ile Pro
200      195      200      205
202 Asp Gly Tyr Lys Ala Ser Arg Pro Ser Gln Glu Asn Phe Ser Leu Ile
203      210      215      220
205 Leu Glu Leu Ala Thr Pro Ser Gln Thr Ser Val Tyr Phe Cys Ala Ser
206 225      230      235      240
208 Gly Glu Thr Gly Thr Asn Glu Arg Leu Phe Phe Gly His Gly Thr Lys
209      245      250      255
211 Leu Ser Val Leu Thr Ser Asn Ser Ile Met Tyr Phe Ser His Phe Val
212      260      265      270
214 Pro Val Phe Leu Pro Ala Lys Pro Thr Thr Thr Pro Ala Pro Arg Pro
215      275      280      285
217 Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro
218      290      295      300
220 Ser Ser Ser Arg Asp Pro Lys Leu Cys Tyr Leu Leu Asp Gly Ile Leu
221 305      310      315      320
223 Phe Ile Tyr Gly Val Ile Leu Thr Ala Leu Phe Leu Arg Val Lys Phe
224      325      330      335
226 Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu
227      340      345      350
229 Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp
230      355      360      365
232 Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys
233      370      375      380
235 Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala
236 385      390      395      400
238 Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys
239      405      410      415
241 Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr
242      420      425      430
244 Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
245      435      440
248 <210> SEQ ID NO: 3
249 <211> LENGTH: 24
250 <212> TYPE: DNA
251 <213> ORGANISM: Artificial Sequence
253 <220> FEATURE:
254 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
256 <400> SEQUENCE: 3
257 cccaaggcac tgatgttcac cttc 24
260 <210> SEQ ID NO: 4
261 <211> LENGTH: 27
262 <212> TYPE: DNA
263 <213> ORGANISM: Artificial Sequence
265 <220> FEATURE:
266 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
268 <400> SEQUENCE: 4
269 tgagacaaag tcccaatct ctgacag 27
272 <210> SEQ ID NO: 5

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Input Set : A:\4835579d.app

Output Set: N:\CRF4\01272004\I774681A.raw

273 <211> LENGTH: 26
274 <212> TYPE: DNA
275 <213> ORGANISM: Artificial Sequence
277 <220> FEATURE:
278 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
280 <400> SEQUENCE: 5
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284 <210> SEQ ID NO: 6
285 <211> LENGTH: 28
286 <212> TYPE: DNA
287 <213> ORGANISM: Artificial Sequence
289 <220> FEATURE:
290 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
292 <400> SEQUENCE: 6
293 tcccggagaa ggtccacagt tcctcttt 28
296 <210> SEQ ID NO: 7
297 <211> LENGTH: 29
298 <212> TYPE: DNA
299 <213> ORGANISM: Artificial Sequence
301 <220> FEATURE:
302 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
304 <400> SEQUENCE: 7
305 gaagcagcag agggtttgaa gccacatac 29
308 <210> SEQ ID NO: 8
309 <211> LENGTH: 27
310 <212> TYPE: DNA
311 <213> ORGANISM: Artificial Sequence
313 <220> FEATURE:
314 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
316 <400> SEQUENCE: 8
317 ggcaggtctt cagttgctta tgaaggt 27
320 <210> SEQ ID NO: 9
321 <211> LENGTH: 27
322 <212> TYPE: DNA
323 <213> ORGANISM: Artificial Sequence
325 <220> FEATURE:
326 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
328 <400> SEQUENCE: 9
329 ggttcctctt cagggtccag aatatgt 27
332 <210> SEQ ID NO: 10
333 <211> LENGTH: 27
334 <212> TYPE: DNA
335 <213> ORGANISM: Artificial Sequence
337 <220> FEATURE:
338 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
340 <400> SEQUENCE: 10
341 gcgaagaact caccctggac tgttcat 27
344 <210> SEQ ID NO: 11
345 <211> LENGTH: 30

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 01/27/2004
PATENT APPLICATION: US/09/774,681A TIME: 13:13:00

Input Set : A:\4835579d.app
Output Set: N:\CRF4\01272004\I774681A.raw

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VERIFICATION SUMMARY

DATE: 01/27/2004

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